

Barb O'Brien

140693 = 4-9

U.S. DEPARTMENT OF COMMERCE
Patent and Trademark Office

SEARCH REQUEST FORM

142410 = text

Requestor's

Name:

My-Chan Team

Serial

Number:

09/380,447

Date:

12/17/04

Phone:

272-0810

Art Unit:

1639

mail box: REM 02405

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

Mrs. O'Brien,

Please search claim 1 ->
and the following
limitations:

- 1) The major coat protein is a M13 filamentous phage (SEQ ID No. 2)
- 2) Its variants are as follows:

~~sequence~~

- 3) The heterologous polypeptide is an antibody that bind to a target, which is exb2.
- 4) The heterologous polypeptide is link to the major coat protein by a linking peptide of SEQ ID No. 110

Thanks ☺

S. Sidhu G. Weiss J. Wells Mod. of coat protein

STAFF USE ONLY

Date completed: 1-12-05
Searcher: PSB
Terminal time: 25 55
Elapsed time: 20 30
CPU time: _____
Total time: _____
Number of Searches: _____
Number of Databases: _____

Search Site

_____ STIC

_____ CM-1

_____ Pre-S

Type of Search

_____ N.A. Sequence

4 A.A. Sequence

_____ Structure

X Bibliographic

Vendors

_____ IG Suite

218/300 STN

_____ Dialog

_____ APS

_____ Geninfo

_____ SDC

_____ DARC/Questel

_____ Other

=> fil reg; d que 110
FILE 'REGISTRY' ENTERED AT 09:39:33 ON 12 JAN 2005
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Property values tagged with IC are from the ZIC/VINITI data file
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STRUCTURE FILE UPDATES: 10 JAN 2005 HIGHEST RN 811411-12-8
DICTIONARY FILE UPDATES: 10 JAN 2005 HIGHEST RN 811411-12-8

TSCA INFORMATION NOW CURRENT THROUGH MAY 21, 2004

Please note that search-term pricing does apply when
conducting SmartSELECT searches.

Crossover limits have been increased. See HELP CROSSOVER for details.

Experimental and calculated property data are now available. For more
information enter HELP PROP at an arrow prompt in the file or refer
to the file summary sheet on the web at:
<http://www.cas.org/ONLINE/DBSS/registryss.html>

L10 13: SEA FILE=REGISTRY ABB=ON [AD][EK][GS][DE][DK][PF][AS][KR][AD]A
[FY][NE][SA]L[QE][AD][SI][AI]T[EN][YL][IF][GF][YL][AL][WG][AT][
MV][VY]VVIVGATIGIKLFFKFTSKAS/SQSFP
*Seg 2, allowing for
specified variations
+ conservative
substitutions
at the other
positions*

=> d rn cn sql kwic nte lc 110 1-13

L10 ANSWER 1 OF 13 REGISTRY COPYRIGHT 2005 ACS on STN
RN 799856-67-0 REGISTRY - *Use Registry # to match sequence to citation (beginning on pg 6)*
CN 7: PN: WO2004101608 SEQID: 7 unclaimed protein (9CI) (CA INDEX NAME)
SQL 77

SEQ 1 SGTAMADPNR FRGKDLAGSP GGGSGGGAEG DDPKAAAFNS LQASATEYIG
=====

51 YAWAMVVVIV GATIGIKLFFK KFTSKAS
=====

HITS AT: 28-77

RELATED SEQUENCES AVAILABLE WITH SEQLINK
LC STN Files: CA, CAPLUS, TOXCENTER

L10 ANSWER 2 OF 13 REGISTRY COPYRIGHT 2005 ACS on STN
RN 685484-38-2 REGISTRY
CN GenBank AAT27365 (9CI) (CA INDEX NAME) *GenBank records
printed at yellow tabs*
OTHER NAMES:
CN GenBank AAT27365 (Translated from: GenBank AY598820)
SQL 73

SEQ 1 MKKSLVLKAS VAVATLVPML SFAAEGDDPA KAAFNSLQAS ATEYIGYAWA
=====

51 MVVVIVGATI GIKLFFKFTS KAS
=====

HITS AT: 24-73

RELATED SEQUENCES AVAILABLE WITH SEQLINK

L10 ANSWER 3 OF 13 REGISTRY COPYRIGHT 2005 ACS on STN
RN 480506-95-4 REGISTRY

CN GenBank CAA23861 (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank CAA23861 (Translated from: GenBank V00604)
SQL 73

SEQ 1 MKKSLVLKAS VAVATLVPML SFAAEGDDPA KAAFNSLQAS ATEYIGYAWA
=====

51 MVVVIVGATI GIKLFKKFTS KAS
=====

HITS AT: 24-73

RELATED SEQUENCES AVAILABLE WITH SEQLINK

L10 ANSWER 4 OF 13 REGISTRY COPYRIGHT 2005 ACS on STN

RN 460400-92-4 REGISTRY

CN L-Serine, L-alanyl-L- α -glutamylglycyl-L- α -aspartyl-L- α -
aspartyl-L-prolyl-L-alanyl-L-lysyl-L-alanyl-L-alanyl-L-phenylalanyl-L-
asparaginyl-L-seryl-L-leucyl-L-glutamyl-L-alanyl-L-seryl-L-alanyl-L-
threonyl-L- α -glutamyl-L-tyrosyl-L-isoleucylglycyl-L-tyrosyl-L-alanyl-
L-tryptophyl-L-alanyl-L-methionyl-L-valyl-L-valyl-L-valyl-L-isoleucyl-L-
valylglycyl-L-alanyl-L-threonyl-L-isoleucylglycyl-L-isoleucyl-L-lysyl-L-
leucyl-L-phenylalanyl-L-lysyl-L-lysyl-L-phenylalanyl-L-threonyl-L-seryl-L-
lysyl-L-alanyl- (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 3: PN: WO02072780 SEQID: 10 unclaimed protein

SQL 50

SEQ 1 AEGDDPAKAA FNSLQASATE YIGYAWAMVV VIVGATIGIK LFKKFTSKAS
=====

HITS AT: 1-50

RELATED SEQUENCES AVAILABLE WITH SEQLINK

LC STN Files: CA, CAPLUS, TOXCENTER, USPATFULL

L10 ANSWER 5 OF 13 REGISTRY COPYRIGHT 2005 ACS on STN

RN 405053-51-2 REGISTRY

CN L-Serine, L-alanyl-L- α -glutamylglycyl-L- α -aspartyl-L- α -
aspartyl-L-prolyl-L-alanyl-L-lysyl-L-alanyl-L-alanyl-L-phenylalanyl-L-
asparaginyl-L-seryl-L-leucyl-L-glutamyl-L-alanyl-L-seryl-L-alanyl-L-
threonyl-L- α -glutamyl-L-tyrosyl-L-isoleucylglycyl-L-tyrosyl-L-alanyl-
L-tryptophyl-L-alanyl-L-methionyl-L-valyl-L-valyl-L-valyl-L-isoleucyl-L-
valylglycyl-L-alanyl-L-threonyl-L-isoleucylglycyl-L-isoleucyl-L-lysyl-L-
leucyl-L-phenylalanyl-L-lysyl-L-lysyl-L-phenylalanyl-L-threonyl-L-seryl-L-
lysyl-L-alanyl- (9CI) (CA INDEX NAME)

SQL 50

SEQ 1 AEGDDPAKAA FNSLQASATE YIGYAWAMVV VIVGATIGIK LFKKFTSKAS
=====

HITS AT: 1-50

RELATED SEQUENCES AVAILABLE WITH SEQLINK

LC STN Files: CA, CAPLUS

L10 ANSWER 6 OF 13 REGISTRY COPYRIGHT 2005 ACS on STN

RN 346502-45-2 REGISTRY

CN 21: PN: US6251865 SEQID: 21 unclaimed protein (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 1: PN: WO0187323 PAGE: 39 unclaimed sequence

SQL 77

SEQ 1 SGTAMADPNR FRGKDLGASP GGGSGGGAEG DDPKAAAFNS LQASATEYIG
=====

51 YAWAMVVVIV GATIGIKLFK KFTSKAS

=====

HITS AT: 28-77

RELATED SEQUENCES AVAILABLE WITH .SEQLINK

LC STN Files: CA, CAPLUS, TOXCENTER, USPATFULL

L10 ANSWER 7 OF 13 REGISTRY COPYRIGHT 2005 ACS on STN
RN 316203-10-8 REGISTRY
CN Protein A (synthetic Staphylococcus aureus clone pAlg-816 precursor
N-terminal fragment) fusion protein with immunoglobulin, anti-(Z-DNA)
(mouse single-chain) fusion protein with protein (coliphage M13 gene III
coat C-terminal fragment) (9CI) (CA INDEX NAME)
SQL 364

SEQ 301 KLEIKHHHHH GSGTAEGDDP AKAAFNSLQA SATEYIGYAW AMVVVIVGAT
=====

351 IGIKLFKKFT SKAS
=====

HITS AT: 315-364

LC STN Files: CA, CAPLUS

L10 ANSWER 8 OF 13 REGISTRY COPYRIGHT 2005 ACS on STN
RN 151033-87-3 REGISTRY
CN (1-6)-(9-21)-Phosphatase, alkaline (Escherichia coli precursor reduced)
fusion protein with trypsin inhibitor (cattle pancreas basic reduced)
fusion protein with protein (coliphage M13 coat) (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN (1-6)-(9-21)-Phosphatase, alkaline (Escherichia coli precursor reduced)
fusion protein with trypsin inhibitor (ox pancreas basic reduced) fusion
protein with protein (coliphage M13 coat)
OTHER NAMES:
CN (1-6)-(9-21)-Phosphatase, alkaline (Escherichia coli precursor reduced)
fusion protein with trypsin inhibitor (ox pancreas basic reduced) fusion
protein with protein (bacteriophage M13 coat)
SQL 127

SEQ 51 TFVYGGCRAK RNNFKSAEDC MRTCGGAAEG DDPAKAAFNS LQASATEYIG
=====

101 YAWAMVVVIV GATIGIKLFK KFTSKAS
=====

HITS AT: 78-127

LC STN Files: CA, CAPLUS, TOXCENTER, USPATFULL

L10 ANSWER 9 OF 13 REGISTRY COPYRIGHT 2005 ACS on STN
RN 144999-51-9 REGISTRY
CN Trypsin inhibitor (cattle pancreas basic reduced), (58→1')-protein
with protein (coliphage M13 coat) (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN Trypsin inhibitor (ox pancreas basic reduced), (58→1')-protein with
protein (coliphage M13 coat)
OTHER NAMES:
CN Trypsin inhibitor (ox pancreas basic reduced), (58→1')-protein with
protein (bacteriophage M13 coat)
SQL 108

SEQ 51 CMRTCGGAAE GDDPAKAAFN SLQASATEYI GYAWAMVVVI VGATIGIKLF
=====

101 KKFTSKAS
=====

HITS AT: 59-108

LC STN Files: CA, CAPLUS, TOXCENTER

L10 ANSWER 10 OF 13 REGISTRY COPYRIGHT 2005 ACS on STN

RN 144999-50-8 REGISTRY
CN 1-21-Phosphatase, alkaline (Escherichia coli precursor reduced),
(21→1')-protein with trypsin inhibitor (cattle pancreas basic
reduced) (58'→1'')-protein with protein (coliphage M13 coat) (9CI)
(CA INDEX NAME)
OTHER CA INDEX NAMES:
CN 1-21-Phosphatase, alkaline (Escherichia coli precursor reduced),
(21→1')-protein with trypsin inhibitor (ox pancreas basic reduced)
(58'→1'')-protein with protein (coliphage M13 coat)
OTHER NAMES:
CN 1-21-Phosphatase, alkaline (Escherichia coli precursor reduced),
(21→1')-protein with trypsin inhibitor (ox pancreas basic reduced)
(58'→1'')-protein with protein (bacteriophage M13 coat)
SQL 129

SEQ 51 CQTFVYGGCR AKRNNFKSAE DCMRTCGGAA EGDDPAKAAF NSLQASATEY
=====

101 IGYAWAMVVV IVGATIGIKL.FKKFTSKAS
=====

HITS AT: 80-129
LC STN Files: CA, CAPLUS, TOXCENTER

L10 ANSWER 11 OF 13 REGISTRY COPYRIGHT 2005 ACS on STN
RN 114013-90-0 REGISTRY
CN 1-142-Kinase (phosphorylating), ribulo- (Salmonella typhimurium reduced)
142-glycine-, (142→11')-protein with 11-73-protein (coliphage M13
gene 8) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 1-142-Kinase (phosphorylating), ribulo- (Salmonella typhimurium reduced)
142-glycine-, (142→11')-protein with 11-73-protein (bacteriophage
M13 gene 8)
SQL 205

SEQ 151 MLSFAAEGDD PAKAAFNLSLQ ASATEYIGYA WAMVVVIVGA TIGIKLFKKF
=====

201 TSKAS
=====

HITS AT: 156-205
LC STN Files: CA, CAPLUS

L10 ANSWER 12 OF 13 REGISTRY COPYRIGHT 2005 ACS on STN
RN 104364-70-7 REGISTRY
CN Protein (coliphage M13 coat) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 2: PN: WO0006717 SEQID: 2 unclaimed protein
CN Protein (bacteriophage M13 coat)
SQL 50

SEQ 1 AEGDDPAKAA FNSLQASATE YIGYAWAMVV VIVGATIGIK LFKKFTSKAS
=====

HITS AT: 1-50

****RELATED SEQUENCES AVAILABLE WITH SEQLINK****
LC STN Files: CA, CAPLUS, TOXCENTER

L10 ANSWER 13 OF 13 REGISTRY COPYRIGHT 2005 ACS on STN
RN 76560-64-0 REGISTRY
CN Protein (coliphage M13 coat precursor) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN Protein (bacteriophage M13 coat precursor)
SQL 73

SEQ 1 MKKSLVLKAS VAVATLVPML SFAAEGDDPA KAAFNSLQAS ATEYIGYAWA

=====

51 MVVVIVGATI GIKLFKKFTS KAS

=====

HITS AT: 24-73

RELATED SEQUENCES AVAILABLE WITH SEQLINK

LC STN Files: CA, CAPLUS

=> => fil capl; s l10

FILE 'CAPLUS' ENTERED AT 09:40:26 ON 12 JAN 2005

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*Registry file
answers set
crossed into bibliographic
files to get citations*

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FILE COVERS 1907 - 12 Jan 2005 VOL 142 ISS 3

FILE LAST UPDATED: 10 Jan 2005 (20050110/ED)

This file contains CAS Registry Numbers for easy and accurate substance identification.

'OBI' IS DEFAULT SEARCH FIELD FOR 'CAPLUS' FILE

L15 12 L10

=> fil uspatf toxcenter; s l10

FILE 'USPATFULL' ENTERED AT 09:40:36 ON 12 JAN 2005

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FILE 'TOXCENTER' ENTERED AT 09:40:36 ON 12 JAN 2005

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L16 9 L10

=> dup rem l15,l16

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PROCESSING COMPLETED FOR L15

PROCESSING COMPLETED FOR L16

L17 13 DUP REM L15 L16 (8 DUPLICATES REMOVED)

ANSWERS '1-12' FROM FILE CAPLUS

ANSWER '13' FROM FILE USPATFULL

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 12, 2005, 10:08:53 ; Search time 115 seconds
(without alignments)
187.163 Million cell updates/sec

Title: SEQ110-THEN-SEQ2
Perfect score: 304
Sequence: 1 AMERIDAPFEGDDPAKAA.....VIVGATIGKLFKRTSRAS 60

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.1

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: A_Geneseq_23Sep04:*

1: geneeqp1980s:*\n2: geneeqp1990s:*\n3: geneeqp2000s:*\n4: geneeqp2001s:*\n5: geneeqp2002s:*\n6: geneeqp2003as:*\n7: geneeqp2003bs:*\n8: geneeqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, between and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	250.1	82.3	131	2	AAR04004
2	249	81.9	73	2	AAR04003
3	248	81.6	50	2	AAR040175
4	248	81.6	50	5	ABJ15250
5	248	81.6	77	2	AAW67493
6	248	81.6	77	4	AAW63727
7	248	81.6	77	5	AAW48216
8	248	81.6	77	7	ADD84797
9	248	81.6	77	7	ADD848110
10	248	81.6	77	8	ADP47503
11	248	81.6	77	8	ADG39549
12	248	81.6	77	8	ADG39549
13	248	81.6	77	8	ADG39549
14	248	81.6	77	8	ADG39549
15	248	81.6	77	8	ADG39549
16	248	81.6	77	8	ADG39549
17	248	81.6	77	8	ADG39549
18	248	81.6	77	8	ADG39549
19	248	81.6	77	8	ADG39549
20	242.7	79.8	71	6	ADL08228
21	234	77.0	72	3	AAV94389
22	233.9	76.9	49	2	AAV94389
23	233	76.6	132	3	AAV81275
24	229	75.3	73	7	ADD14860
25	226.1	74.4	79	8	ADP64647

26	93	30.6	20	7	ADM34212	Adm34212 Synthetic
27	88	28.9	24	7	ABR83076	Ab-83076 Major coa
28	71.4	23.5	625	5	ABP65108	Abp65108 Hypoxia-1
29	71.4	23.5	625	8	ADD14192	Add14192 Human src
30	71.4	23.5	625	8	ADN04317	Adn04317 Antipsoi
31	71.4	23.5	653	7	ADJ70738	Adj70738 Human hea
32	71.4	23.5	677	7	ADP09955	Adp09955 Novel pro
33	69.1	22.7	491	4	AAQ91147	Aaq91147 C. glutam
34	69.1	22.7	533	7	ADL65983	Adl65983 C. glutam
35	67.9	22.3	618	4	ABB62317	Abb62317 Drosophi
36	67.8	22.3	303	7	ABG09795	Abg09795 Novel hum
37	67.6	22.2	476	5	ADH86191	Adh86191 Enterococ
38	66.9	22.0	476	8	ADJ49077	Adj49077 Hericicia
39	66.9	22.0	476	8	ADJ49077	Adj49077 Oil-asso
40	66.9	22.0	480	8	ADJ49984	Adj49984 Oil-asso
41	66.9	22.0	480	8	ADJ50237	Adj50237 Oil-asso
42	66.3	21.8	464	3	AAQ18633	Aaq18633 Arabidops
43	66.3	21.8	464	3	AAQ18633	Aaq18633 Arabidops
44	66.3	21.8	496	3	AAQ18632	Aaq18632 Arabidops
45	66.3	21.8	496	3	AAQ18632	Aaq18632 Arabidops

ALIGNMENTS

RESULT 1
AAR04004 standard; protein; 131 AA.

30-SEP-1990 (first entry)

Portion of M13 coat protein with bovine pancreatic trypsin inhibitor insert.

Binding proteins; M13cp-BPPI fusion gene; horse heart myoglobin;

Potential binding domain.

Synthetic.

Key Location/Qualifiers
Region 24..81
FT /label= BPPI sequence

W09002809-A.

22-MAR-1990.

02-SEP-1988; 88US-00240160.

02-SEP-1988; 88US-00240160.

(PROT-) PROTEIN ENG CORP.

Ladner RC, Guterman SK;

WPI; 1990-115996/15.

Prepn. of proteins which bind predetermined target - by generation and selection of recombinant varied binding proteins using replicable genetic packages.

Disclosure; Page 133; 26pp; English.

An insert is made into the M13 coat protein whereby the phage will present a binding domain as a surface protein. That sequence is specifically of the bovine pancreatic trypsin inhibitor (BPPI) which has affinity for an horse heart myoglobin target protein. See also AA003954-58

Sequence 131 AA;

Wed Jan 12 12:35:24 2005

seq110-ther

Wed Jan 12 12:35:24 2005

seq110-th

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GenCore version 5.1.6
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OM protein - protein search, using sw model

OM protein - protein search, using sw model

Run on: January 12, 2005, 10:43:39 ; Search time 28 Seconds
(without alignments)
142.110 Million cell updates/sec

Run on: January 12, 2005, 11:00:20 ; Search time 97.5 Seconds
(without alignments)
222.332 Million cell updates/sec

Title: SEQ110-THEN-SEQ2
Perfect score: 304
Sequence: 1 AMEENIDSAPEAGDDPAKAA.....VIVGATIGIKLKKFTSKAS 60

Title: SEQ110-THEN-SEQ2
Perfect score: 304
Sequence: 1 AMEENIDSAPEAGDDPAKAA.....VIVGATIGIKLKKFTSKAS 60

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.1

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.1

Searched: 478139 seqs, 6631800 residues

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 478139

Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA.*

Database : Published Applications_AA.*

1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/Backfilltest1.pep.*

1: /cgn2_6/ptodata/1/pubppa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubppa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubppa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubppa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubppa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubppa/PCTUS_NEW_PUB.pep.*
7: /cgn2_6/ptodata/1/pubppa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubppa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubppa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubppa/US09C_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubppa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubppa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubppa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubppa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubppa/US10D_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubppa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubppa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	248	81.6	50	1	US-08-133-011-17
2	248	81.6	50	1	US-08-322-730A-17
3	248	81.6	50	1	US-08-387-874-17
4	248	81.6	50	2	US-08-383-619-17
5	248	81.6	50	3	US-08-907-739-17
6	248	81.6	50	4	US-09-729-597-17
7	248	81.6	50	5	PCT-US93-08364-17
8	248	81.6	77	3	US-08-825-852-21
9	248	81.6	77	3	US-09-052-888-21
10	248	81.6	77	4	US-09-723-890-21
11	248	81.6	77	4	US-09-723-901-21
12	248	81.6	77	4	US-09-723-547-21
13	248	81.6	77	4	US-09-724-127-21
14	248	81.6	77	4	US-09-723-931-21
15	248	81.6	77	4	US-09-723-873-21
16	248	81.6	77	4	US-09-724-114-21
17	248	81.6	77	4	US-09-723-913-21
18	248	81.6	77	4	US-09-723-912-21
19	248	81.6	77	4	US-09-724-095-21
20	248	81.6	77	4	US-09-724-157-21
21	248	81.6	77	4	US-09-724-062-21
22	248	81.6	77	4	US-09-724-065-21
23	244	80.3	73	4	US-09-495-880A-9
24	244	80.3	73	4	US-09-495-880A-9
25	244	80.3	73	4	US-09-495-880A-24
26	234	77.0	72	4	US-09-866-073A-17
27	71.4	23.5	625	4	US-09-538-092-1064

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	255	83.9	80	16	US-10-416-708A-57
2	250.1	82.3	127	10	US-09-896-095-270
3	250.1	82.3	131	10	US-09-896-095-187
4	250.1	82.3	131	10	US-09-896-095-268
5	250.1	82.3	131	10	US-09-896-095-273
6	250.1	82.3	132	10	US-09-896-095-220
7	250.1	82.3	132	10	US-09-896-095-222
8	250.1	82.3	132	10	US-09-896-095-224
9	249	81.9	73	10	US-09-896-095-112
10	248	81.6	50	14	US-10-098-093-10
11	248	81.6	50	15	US-10-273-973-17
12	248	81.6	77	10	US-09-858-935B-2
13	248	81.6	77	10	US-09-858-935B-55

Wed Jan 12 12:35:25 2005

seq110-the1

Wed Jan 12 12:35:25 2005

seq110-th

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OM protein - protein search, using sw model

OM protein - protein search, using sw model

Run on: January 12, 2005, 10:11:18 ; Search time 126 Seconds
(without alignments)
273.988 Million cell updates/sec

Run on: January 12, 2005, 10:42:14 ; Search time 24.5 Seconds
(without alignments)
235.633 Million cell updates/sec

Title: SEQ110-THEN-SEQ2

Perfect score: 304

Sequence: 1 AMENIDSPAPAEGLDPAKAA.....VIVGATTGKLFKKFTSKAS 60

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.1

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	244	80.3	73	1	COAB_BPFD	P03617 bacterioph
2	243	79.9	50	2	O9T0Q9	P03618 bacterioph
3	238	78.3	50	1	COAB_BPZJ2	P03619 bacterioph
4	206	67.8	65	2	O38211	P03619 bacterioph
5	173.7	57.1	74	1	COAB_BP1F1	P15416 bacterioph
6	97	31.9	84	1	COAB_BP122	P03620 bacterioph
7	93	30.6	53	2	O9T0Q8	P03620 bacterioph
8	90	29.6	82	1	COAB_BP1KE	O9F4d4 burkholderi
9	75.2	24.7	183	2	O9F4D4	O615x9 oryza sativ
10	75.1	24.7	1070	2	O615X9	O9A3A6 caulobacter
11	73.5	24.2	476	2	O9A3A6	O9A3A6 caulobacter
12	72.8	23.9	351	1	YES5_THEAC	O9A187 thermoplas
13	71.7	23.6	535	2	O55577	O55577 synchocyst
14	71.4	23.5	522	2	O8C514	O8C514 mus musculu
15	71.4	23.5	504	2	O60786	O60786 mus musculu
16	71.4	23.5	540	2	O81187	O81187 mus musculu
17	71.4	23.5	653	1	M1A1_HUMAN	P33308 homo sapien
18	71.4	23.5	1031	2	O8EFT4	O8EFT4 shewanella
19	71.1	23.4	228	2	O7J038	O7J038 mycobacteri
20	71.1	23.4	228	2	AA606080	AA606080 mycobacte
21	70.7	23.3	2167	2	O92EKS	O92EKS listeria in
22	70.3	23.1	400	2	O89114	O89114 bradyrhizob
23	70.2	23.1	436	2	O892A4	O892A4 bacteroides
24	70.2	23.1	499	2	O7JPI6	O7JPI6 treponema d
25	70.2	23.1	499	2	AA611474	AA611474 treponema
26	69.9	23.0	700	2	O7NSA1	O7NSA1 chromobacte
27	69.5	22.9	236	2	O89ED0	O89ED0 bradyrhizob
28	69.4	22.8	523	2	O7VBS1	O7VBS1 prochlorococ
29	69.4	22.8	1285	2	O6Y132	O6Y132 lactuca sat
30	69.4	22.8	1285	2	AAQ72578	AAQ72578 lactuca s
31	69.3	22.8	710	2	O6C6N0	O6C6N0 yarrowia li

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	249	81.9	73	1	VCBPM3	coat protein B pre
2	244	80.3	73	1	VCBPF1	coat protein B pre
3	244	80.3	73	1	VCBPF2	coat protein B pre
4	238	78.3	50	1	VCBPF2	coat protein B pre
5	170.6	56.1	51	1	VCBPF1	coat protein B pre
6	97	31.9	84	2	S08090	gene VIII protein
7	90	29.6	82	1	VCBPF1	coat protein B pre
8	73.5	24.2	476	2	H87657	conserved hypochet
9	71.7	23.6	535	2	S76103	hypochetrical prote
10	71.4	23.5	504	2	I49257	hypochetrical prote
11	71.4	23.5	625	2	S38965	hypochetrical prote
12	70.7	23.3	2167	2	AF1489	mannosyl-oligosac
13	69.1	22.7	419	2	T19260	cell wall-associat
14	68	22.4	513	2	T35899	hypochetrical prote
15	68	22.4	520	2	T35899	hypochetrical prote
16	67.9	22.3	2139	2	AA5672	cytochrome-c oxida
17	67.6	22.2	446	2	S26965	crumbe protein - f
18	67.9	22.0	475	2	C96505	MADH oxidase - Ent
19	66.4	22.0	475	2	D70799	probable amino aci
20	66.4	21.8	369	1	A23559	hypochetrical prote
21	65.7	21.6	317	2	F87634	dihydrooxalate oxi
22	65.7	21.6	411	2	C57479	conserved hypochet
23	65.6	21.6	598	2	T50288	amino acid transpo
24	65.5	21.5	388	2	T45081	probable transmemo
25	65.2	21.4	5149	2	F83345	3-ketoacyl-CoA thi
26	65	21.4	400	2	C85882	permease of transp
27	64.9	21.4	400	2	H91037	permease of transp
28	64.9	21.3	910	2	JC4609	chitin synthase (E
29	64.9	21.3	1331	2	T18310	receptor-adenylate